

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 8, 2003, 14:33:07 ; Search time 47 seconds
(Without alignments)

1114.750 Million cell updates/sec

Title: US-09-001-737-8

Perfect score: 545
Sequence: 1 MAKEIKFSADARAAMVRCVD.....TPAPAMPAGMDPMGMKGNG 545

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 8

Total number of hits satisfying chosen parameters: 191

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

PIR_73:.*
1: PIR1:.*
2: PIR2:.*
3: PIR3:.*
4: PIR4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	70	12.8	540	2	G95222
2	70	12.8	540	2	H88086
3	56	10.3	542	2	B86574
4	31	5.7	542	2	A01333
5	27	5.0	544	2	B36917
6	27	5.0	544	2	S23918
7	27	5.0	544	2	B97442
8	27	5.0	544	2	A02660
9	27	5.0	545	2	JN0509
10	27	5.0	545	2	S47530
11	27	5.0	545	2	C95311
12	27	5.0	547	2	I40331
13	26	4.8	538	2	C89994
14	26	4.8	539	2	JN0601
15	26	4.8	541	2	JN0512
16	26	4.8	542	2	F95967
17	26	4.8	542	2	A01704
18	25	4.6	539	2	B49855
19	25	4.6	541	2	S68249
20	25	4.6	542	2	JN0651
21	25	4.6	542	2	S92106
22	25	4.6	544	2	J05130
23	25	4.6	544	2	J06063
24	25	4.6	544	2	B83720
25	24	4.4	538	2	J01195
26	24	4.4	544	2	A71555
27	24	4.4	544	2	B41884
28	24	4.4	544	2	S19023
29	24	4.4	544	2	I40731

30	24	4.4	544	2	JT0117	hyB protein - Chl
31	24	4.4	544	2	B41479	60K heat shock pro
32	24	4.4	544	2	F86507	heat shock protein
33	24	4.4	544	2	B81556	60 kDa chaperonin
34	24	4.4	544	2	D81709	60 kDa chaperonin
35	24	4.4	544	2	A02263	chaperonin groEL (
36	24	4.4	545	2	G81328	60 kD chaperonin
37	24	4.4	546	2	I40342	heat shock protein
38	24	4.4	546	2	S22347	groEL - Brucella a
39	23	4.2	543	2	B41872	heat shock protein
40	23	4.2	543	2	F97232	chaperonin groEL
41	23	4.2	544	2	S70667	chaperonin groEL -
42	23	4.2	545	2	S51563	heat shock protein
43	23	4.2	546	2	B47073	chaperonin groEL -
44	23	4.2	547	2	B43606	heat shock protein
45	23	4.2	547	2	B87334	chaperonin, 60 kDa
46	23	4.2	547	2	B83098	groEL protein PA43
47	22	4.0	544	1	B43827	chaperonin groEL -
48	22	4.0	546	2	A03840	60K chaperonin gro
49	22	4.0	549	2	J02564	heat shock protein
50	22	4.0	585	2	S49253	rubisco binding pr
51	21	3.9	541	2	B44425	chaperonin groEL -
52	21	3.9	541	2	T06829	chaperonin groEL -
53	21	3.9	552	2	S39765	chaperonin 60 - Co
54	20	3.7	540	2	A26950	groEL protein - M
55	20	3.7	540	2	A43509	65K antigen mbaa -
56	20	3.7	541	2	S40245	heat shock protein
57	20	3.7	541	2	T44725	chaperonin 60K (im
58	20	3.7	544	2	S37039	groEL protein - Ba
59	20	3.7	546	2	S65596	heat shock protein
60	20	3.7	588	2	A25902	65K antigen - Myco
61	19	3.5	541	2	JN0511	heat shock protein
62	19	3.5	541	2	S72614	chaperonin 60 - Th
63	19	3.5	544	1	BYVCGI	chaperonin groEL -
64	19	3.5	546	2	S34938	heat shock protein
65	19	3.5	546	2	S35311	heat shock cognate
66	19	3.5	550	2	S35309	heat shock protein
67	17	3.1	539	2	F70737	chaperonin groEL
68	17	3.1	544	2	H95269	GROEL3 Chaperonin
69	17	3.1	547	2	F82783	60KDa chaperonin X
70	16	2.9	539	2	S22342	chaperonin HSP60 -
71	16	2.9	540	2	S37566	groEL protein - S
72	16	2.9	540	2	C41325	heat shock protein
73	16	2.9	540	2	B41325	heat shock protein
74	16	2.9	541	2	S61301	chaperonin cpn60 -
75	16	2.9	541	2	T35591	heat shock protein
76	16	2.9	543	2	D64243	heat shock protein
77	16	2.9	543	2	S73595	heat shock protein
78	16	2.9	544	2	S61302	heat shock protein
79	16	2.9	544	2	S61303	heat shock protein
80	16	2.9	544	2	S61303	heat shock protein
81	16	2.9	544	2	H81964	chaperonin 60K su
82	16	2.9	544	2	C81021	chaperonin, 60 kDa
83	15	2.8	530	2	D82412	chaperonin, 60 kD
84	15	2.8	534	2	S26977	groEL protein - re
85	15	2.8	543	2	J05771	chaperonin groEL-1
86	15	2.8	544	2	B82048	chaperonin, 60 kD
87	15	2.8	545	2	H70180	heat shock protein
88	15	2.8	546	2	B54539	heat shock protein
89	15	2.8	547	2	J04519	heat shock protein
90	15	2.8	547	2	B49203	heat shock protein
91	15	2.8	548	1	BVEGCL	chaperonin groEL -
92	15	2.8	548	2	C64076	chaperonin groEL -
93	15	2.8	548	2	B42281	chaperonin groEL -
94	15	2.8	548	2	D81289	chaperonin symL p
95	15	2.8	548	2	B84932	chaperonin groEL (
96	15	2.8	548	2	B86110	60 kD chaperonin
97	15	2.8	548	2	AG0043	hypothetical prote
98	15	2.8	548	2	AE1045	60 kDa chaperonin
99	15	2.8	550	2	S52901	groEL protein (imp
100	15	2.8	550	2	S26423	heat shock protein
101	15	2.8	550	2	A41468	heat shock protein
102	15	2.8	551	2	J02562	60K heat shock pro

103	15	2.8	569	2	S11035	chaperonin hsp60,
104	15	2.8	573	1	A32800	chaperonin groEL p
105	15	2.8	573	1	HHRT60	chaperonin groEL p
106	15	2.8	573	1	HHMS60	chaperonin groEL p
107	15	2.8	573	2	A34173	chaperonin groEL p
108	15	2.6	435	2	S56644	chaperonin 60 beta
109	14	2.6	528	2	S73270	chaperonin 60 beta
110	14	2.6	528	2	S73270	chaperonin 60 beta
111	14	2.6	528	2	S73270	chaperonin 60 beta
112	14	2.6	537	2	S25181	chaperonin 60 - Od
113	14	2.6	538	2	H72367	heat shock protein
114	14	2.6	543	2	S70013	chaperonin-like pr
115	14	2.6	548	2	H97820	60k chaperonin (lm
116	14	2.6	550	2	A71668	chaperonin groEL-2
117	14	2.6	552	2	S74322	heat shock protein
118	14	2.6	572	2	J00157	heat shock protein
119	14	2.6	574	2	T49325	probable heat-shoc
120	13	2.4	174	2	T07736	probable chaperoni
121	13	2.4	544	2	H71374	chaperonin groEL -
122	13	2.4	546	2	S36237	chaperonin groEL -
123	13	2.4	588	2	B71986	chaperonin 62.5K b
124	13	2.4	595	2	T06412	probable chaperoni
125	13	2.4	599	2	T07733	chaperonin 60 beta
126	13	2.4	600	2	JT0901	Rubisco subunit b1
127	13	2.4	600	2	B95597	chaperonin 60 beta
128	12	2.2	259	2	S56466	GroEL - Aquilifex ae
129	12	2.2	545	2	C70489	GroEL protein - De
130	12	2.2	545	2	G73499	heat-shock protein
131	12	2.2	550	2	S61297	58k antigen - Rick
132	12	2.2	555	2	B41492	heat-shock protein
133	12	2.2	582	2	S62335	heat-shock protein
134	12	2.2	582	2	T43369	heat-shock protein
135	12	2.2	589	2	H90112	Cpn60 protein (lmp
136	12	2.2	611	2	E86388	probable chaperoni
137	11	2.0	114	2	S05292	55k antigen - Myco
138	11	2.0	114	2	S05292	55k antigen - Myco
139	11	2.0	114	2	S05292	55k antigen - Myco
140	11	2.0	114	2	S05292	55k antigen - Myco
141	11	2.0	114	2	S05292	55k antigen - Myco
142	11	2.0	114	2	S05292	55k antigen - Myco
143	11	2.0	545	2	PM0008	chaperonin 60k be
144	11	2.0	560	2	AB2043	chaperonin 60k al
145	11	2.0	562	2	S61295	chaperonin groEL (
146	11	2.0	583	2	S38642	heat shock protein
147	11	2.0	586	2	S71235	chaperonin 60 alph
148	10	1.8	16	2	C44896	chaperonin 60 alph
149	10	1.8	495	1	H8CSBA	heat shock protein
150	10	1.8	524	2	PM0008	chaperonin groEL -
151	10	1.8	543	1	HHMTBA	mitochondrial chap
152	10	1.8	575	2	S29315	chaperonin groEL a
153	10	1.8	575	2	S29315	chaperonin 60 - cu
154	10	1.8	576	2	S26583	chaperonin hsp60 -
155	10	1.8	577	2	S26582	chaperonin hsp60 -
156	10	1.8	577	2	S20875	chaperonin hsp60 p
157	10	1.8	577	2	S20875	chaperonin hsp60 p
158	10	1.8	580	2	S56645	chaperonin 60 alph
159	10	1.8	587	2	S38634	chaperonin 60 alph
160	10	1.8	587	2	T06518	chaperonin 60 alph
161	9	1.7	220	2	A75362	chaperonin 60 alph
162	8	1.5	131	2	G82684	hypothetical prote
163	8	1.5	156	2	JT0902	hypothetical prote
164	8	1.5	177	2	PM0374	orif 5'of acvB - A
165	8	1.5	191	2	G81808	chaperonin 60 beta
166	8	1.5	235	2	H71435	hypothetical prote
167	8	1.5	240	2	H71435	probable iron upla
168	8	1.5	333	2	AB2237	hypothetical prote
169	8	1.5	343	2	A93198	phospho-2-dehydro-
170	8	1.5	343	2	E88064	2-dehydro-3-deoxy-
171	8	1.5	355	2	T38483	hypothetical prote
172	8	1.5	391	2	T44839	probable amino-tra
173	8	1.5	431	2	J50055	hypothetical 43.7k
174	8	1.5	441	2	S19606	hydrogenase regula
175	8	1.5	441	2	AB0931	transcription regu

176	8	1.5	524	2	D84718	probable glutamyl
177	8	1.5	543	2	S53817	thermosome beta ch
178	8	1.5	545	2	JC4270	hypethermophilic
179	8	1.5	545	2	B69431	thermosome, subuni
180	8	1.5	545	2	F69529	thermosome, subuni
181	8	1.5	546	2	S61294	heat-shock protein
182	8	1.5	548	2	T43915	chaperonin alpha c
183	8	1.5	549	2	F71219	probable thermophi
184	8	1.5	550	2	F75186	thermosome, chain
185	8	1.5	552	2	H69126	chaperonin - Metha
186	8	1.5	552	2	T47128	heat shock protein
187	8	1.5	556	2	D84359	thermosome subunit
188	8	1.5	700	2	S38426	chaperonin 60 prec
189	8	1.5	851	2	G71435	hypothetical prote
190	8	1.5	1325	2	T01037	hypothetical prote
191	8	1.5	1520	1	TVFPA	protein-tyrosine k

ALIGNMENTS

RESULT 1

G95222 chaperonin, 60 kDa [imported] - Streptococcus pneumoniae (strain TIGR4)

C:Species: Streptococcus pneumoniae
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001C:Accession: G95222
R:Retelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.;on, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzap
Science 293: 498-506, 2001A:Authors: Lotius, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morri
A:Title: Complete Genome Sequence of a Virulent Isolate of Streptococcus pneumoniae.
A:Reference number: A95000; M01D:2157209; PMID:11463916A:Accession: G95222
A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-540 <XPR>
A:Cross-references: GB:AE005672; PIDN:AAK75976.1; PID:g14973411; GSPDB:GN00164; TIGRA:Experimental source: strain TIGR4
A:Genetic: S1906
A:Gene: SP1906C:Superfamily: chaperonin groEL
Query Match 12.8%; Score 70; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 5, 9e-61;Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 242 NRPLIADVDGEALPTLVKIRGTENVAVAPGFGRRKAMEDIAITLGTGTYTE 301

DB 242 NRPLIADVDGEALPTLVKIRGTENVAVAPGFGRRKAMEDIAITLGTGTYTE 301

QY 302 DLGLEKDAT 311

DB 302 DLGLEKDAT 311

RESULT 2

H98086 chaperonin groEL [imported] - Streptococcus pneumoniae (strain R6)

C:Species: Streptococcus pneumoniae
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001C:Accession: H98086
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; Dehoff, B.S.e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.
y, P.; Sun, P.M.; Winkler, M.E.J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; M01D:21429245; PMID:11544234A:Accession: H98086
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-540 <KUP>
 A:Cross-references: GB:AE007317; PIDN:AL00525.1; PID:g15459401; GSPDB:GN00174
 C:Genetics:
 A:Gene: groEL
 C:Superfamily: chaperonin groEL

Query Match 12.8%; Score 70; DB 2; Length 540;
 Best Local Similarity 100.0%; Pred. No. 5.9e-61;
 Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 NRLLLIADVDGEGALPTLVNKRITGFNVVAVKAPFGDRRRKAMLEDAITLTGTVITE 301
 DB 242 NRLLLIADVDGEGALPTLVNKRITGFNVVAVKAPFGDRRRKAMLEDAITLTGTVITE 301

QY 302 DLGLEIKDAT 311
 DB 302 DLGLEIKDAT 311

RESULT 3
 B86674
 60 KD chaperonin [Imported] - Lactococcus lactis subsp. lactis (strain IL1403)
 C:Species: Lactococcus lactis subsp. lactis
 C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
 C:Accession: B86674
 R:Biological: A.; Mincker, P.; Manger, S.; Jallion, O.; Malarme, K.; Weissenbach, J.; Ehrlich
 A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
 A:Reference number: AB6675; MUID:2135186; PMID:11337471
 A:Accession: B86674
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-542 <STO>
 A:Cross-references: GB:AE005176; PID:g12723267; PIDN:AAK04492.1; GSPDB:GN00146
 A:Experimental source: strain IL1403
 C:Genetics:
 A:Gene: groEL
 C:Superfamily: chaperonin groEL

Query Match 10.3%; Score 56; DB 2; Length 542;
 Best Local Similarity 100.0%; Pred. No. 5e-47;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 GSPITNGVITAKIEIEHDFEMGAKLYSEVASTNDIAGDGTITVLTQAIIV 99
 DB 44 GSPITNGVITAKIEIEHDFEMGAKLYSEVASTNDIAGDGTITVLTQAIIV 99

RESULT 4
 AD1333
 Class I heat-shock protein (chaperonin) GroEL [Imported] - Listeria monocytogenes (strat
 C:Species: Listeria monocytogenes
 C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
 C:Accession: AD1333
 R:Biological: P.; Frangoul, L.; Buchleier, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
 D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl, H.
 A:Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapat, G.; Madueno, E.; Maitournam, A.; M
 Ok, C.; Schueter, T.; Simoes, N.; Tiller, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
 A:Title: Comparative genomics of Listeria species.
 A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: AD1333
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-542 <GLA>
 A:Cross-references: GB:NC_003210; PIDN:CAD00146.1; PID:g16411538; GSPDB:GN00177
 A:Experimental source: strain EGD-e
 C:Genetics:
 A:Gene: groEL
 C:Superfamily: chaperonin groEL

Query Match 5.7%; Score 31; DB 2; Length 542;

Best Local Similarity 100.0%; Pred. No. 3.8e-22;
 Matches 31; Conservative 0; Mismatches 0; Indels 0;

QY 266 RGFNVVAVKAPFGDRRRKAMLEDAITLTGTV 296
 DB 266 RGFNVVAVKAPFGDRRRKAMLEDAITLTGTV 296

RESULT 5
 B36917
 heat shock protein GroEL - Agrobacterium tumefaciens
 C:Species: Agrobacterium tumefaciens
 C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 12-Sep-1997
 C:Accession: B36917
 R:Segal, G.; Kon, E.
 J. Bacteriol. 175, 3083-3088, 1993
 A:Title: Heat shock transcription of the groEL operon of Agrobacterium tumefaciens
 A:Reference number: A36917; MUID:93259955; PMID:8098329
 A:Accession: B36917
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-544 <SEG>
 A:Note: sequence extracted from NCBI backbone (NCBIN:131959, NCBI:131961)
 C:Superfamily: chaperonin groEL

Query Match 5.0%; Score 27; DB 2; Length 544;
 Best Local Similarity 100.0%; Pred. No. 3.7e-18;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 273 AVKAPFGDRRRKAMLEDAITLTGTVI 299
 DB 273 AVKAPFGDRRRKAMLEDAITLTGTVI 301

RESULT 6
 S23918
 groEL protein - Agrobacterium tumefaciens
 C:Species: Agrobacterium tumefaciens
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
 C:Accession: S23918
 R:Segal, G.; Kon, E.
 submitted to the EMBL Data Library, August 1992
 A:Description: Cloning and sequencing of the GroE operon of Agrobacterium tumefacie
 A:Reference number: S23917
 A:Accession: S23918
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-544 <SEG>
 A:Cross-references: EMBL:X68263; NID:g1019913; PIDN:CAA48331.1; PID:g39095
 C:Superfamily: chaperonin groEL

Query Match 5.0%; Score 27; DB 2; Length 544;
 Best Local Similarity 100.0%; Pred. No. 3.7e-18;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 273 AVKAPFGDRRRKAMLEDAITLTGTVI 299
 DB 273 AVKAPFGDRRRKAMLEDAITLTGTVI 301

RESULT 7
 B97442
 60K chaperonin (protein cpn60) (groEL protein) [Imported] - Agrobacterium tumefaciens
 C:Species: Agrobacterium tumefaciens
 C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
 C:Accession: B97442
 R:Goodner, B.; Hinkle, G.; Gattling, S.; Miller, N.; Blanchard, M.;
 A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Le
 Science 294, 2223-2228, 2001
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology
 A:Reference number: A97359; PMID:11743194
 A:Accession: B97442
 A:Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-544 <KUR>
 A:Cross-references: GB:AE007869; PIDN:AAK6491.1; PID:g1515641; GSPDB:GN00169
 C:Genetics:
 A:Gene: AGR_C-1220
 A:Map position: circular chromosome
 C:Superfamily: chaperonin groEL

Query Match 5.0%; Score 27; DB 2; Length 544;
 Best Local Similarity 100.0%; Pred. No. 3.7e-18;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 273 AVKAPGFGDRRKAMLEDAIILTGTVI 299
 ||||||||||||||||||||||||||||||||
 Db 275 AVKAPGFGDRRKAMLEDAIILTGTVI 301

RESULT 8

AD2660
 60 kDa chaperonin [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
 C:Species: Agrobacterium tumefaciens
 C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
 C:Accession: AD2660
 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Moo, I.
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
 Science 294, 2317-2323, 2001
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
 ster, E.W.
 A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:Reference number: AB2577; PMID:11743193
 A:Accession: AD2660
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-544 <KUR>
 A:Cross-references: GB:AE008688; PIDN:AA141698.1; PID:g17739044; GSPDB:GN00186
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: groEL
 A:Map position: circular chromosome
 C:Superfamily: chaperonin groEL

Query Match 5.0%; Score 27; DB 2; Length 544;
 Best Local Similarity 100.0%; Pred. No. 3.7e-18;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 273 AVKAPGFGDRRKAMLEDAIILTGTVI 299
 ||||||||||||||||||||||||||||||||
 Db 275 AVKAPGFGDRRKAMLEDAIILTGTVI 301

RESULT 9

JN0509
 heat shock protein groEL (clone Rhz A) - Rhizobium meliloti
 C:Species: Rhizobium meliloti
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
 C:Accession: JN0509
 R:Rusanganva, E.; Gupta, R.S.
 Gene 126, 67-75, 1993
 A:Title: Cloning and characterization of multiple groEL chaperonin-encoding genes in Rhz
 A:Reference number: JN0509; MUID:93231539; PMID:8091179
 A:Accession: JN0509
 A:Molecule type: DNA
 A:Residues: 1-345 <RUS>
 A:Cross-references: GB:M94192; NID:g152233; PIDN:AAA26285.1; PID:g152235
 C:Comment: This protein plays a role in protein folding and in the extracellular transp
 C:Genetics:
 A:Gene: groEL
 C:Superfamily: chaperonin groEL
 C:Keywords: heat shock; molecular chaperone; stress-induced protein

Query Match 5.0%; Score 27; DB 2; Length 545;

Best Local Similarity 100.0%; Pred. No. 3.7e-18;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 273 AVKAPGFGDRRKAMLEDAIILTGTVI 299
 ||||||||||||||||||||||||||||||||
 Db 275 AVKAPGFGDRRKAMLEDAIILTGTVI 301

RESULT 10

S47530
 chaperonin groEL - Porphyromonas gingivalis
 C:Species: Porphyromonas gingivalis
 C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
 C:Accession: S47530
 R:Hotokezaka, H.; Hayashida, H.; Ohara, N.; Nomaguchi, H.; Kobayashi, K.; Yamada, T.
 Biochim. Biophys. Acta 1219, 175-178, 1994
 A:Title: Cloning and sequencing of the groEL homologue from Porphyromonas gingivalis
 A:Reference number: S47530; MUID:94368851; PMID:8086460
 A:Accession: S47530
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-545 <HOR>
 A:Cross-references: EMBL:D17342; NID:g5324298; PIDN:BA04161.1; PID:g532499
 A:Note: the source is designated as Bacteroides gingivalis
 C:Superfamily: chaperonin groEL

Query Match 5.0%; Score 27; DB 2; Length 545;
 Best Local Similarity 100.0%; Pred. No. 3.7e-18;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 273 AVKAPGFGDRRKAMLEDAIILTGTVI 299
 ||||||||||||||||||||||||||||||||
 Db 275 AVKAPGFGDRRKAMLEDAIILTGTVI 301

RESULT 11

C95311
 groEL2 chaperonin [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSym
 C:Species: Sinorhizobium meliloti
 C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
 C:Accession: C95311
 R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.;
 Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
 A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium mel
 A:Reference number: A95262; MUID:21396509; PMID:11481432
 A:Accession: C95311
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-545 <KUR>
 A:Cross-references: GB:AE006469; PIDN:AAK65053.1; PID:g14523485; GSPDB:GN00165
 A:Experimental source: strain 1021, megaplasmid pSymA
 R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hub
 pela, D.; Chain, P.; Cowle, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R
 L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lela
 heault, P.; Vandenhof, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yen
 A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
 A:Reference number: A96039; MUID:21368234; PMID:11474104
 A:Contents: annotation
 C:Genetics:
 A:Gene: groEL2
 A:Genome: plasmid
 C:Superfamily: chaperonin groEL

Query Match 5.0%; Score 27; DB 2; Length 545;
 Best Local Similarity 100.0%; Pred. No. 3.7e-18;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 273 AVKAPGFGDRRKAMLEDAIILTGTVI 299
 ||||||||||||||||||||||||||||||||
 Db 275 AVKAPGFGDRRKAMLEDAIILTGTVI 301

RESULT 12

CPn60 protein (GroEL) - Bordetella pertussis
C:Species: Bordetella pertussis
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 26-Aug-1999
C:Accession: I40331
R: Fernandez, R.C.; Weiss, A.A.
Gene 158, 151-152, 1995
A:Title: Cloning and sequencing of the Bordetella pertussis cpn60 (groEL) homolog
A:Reference number: I40330; MUID:95309719; PMID:7789805
A:Accession: I40331
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-547 <RES>
A:Cross-References: EMBL:U12277; NID:9968918; PIDN:AAA74967.1; PID:9968920
C:Genetics:
A:Gene: cpn60
C:Superfamily: chaperonin groEL

Query Match 5.0%; Score 27; DB 2; Length 547;
Best Local Similarity 100.0%; Pred. No. 3.7e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 273 AVKAPGFDGRRKAMLEDAITLTGTVI 299
|||||

DB 275 AVKAPGFDGRRKAMLEDAITLTGTVI 301
|||||

RESULT 13

GroEL protein [Imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: C89994
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizutani-U, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratsuka, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: C89994
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-538 <KOR>
A:Cross-References: GB:BA000018; PID:913701823; PIDN:BA843116.1; GSPDB:GNO0149
A:Experimental source: strain N315
C:Genetics:
A:Gene: groEL
C:Superfamily: chaperonin groEL

Query Match 4.8%; Score 26; DB 2; Length 538;
Best Local Similarity 100.0%; Pred. No. 3.6e-17;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 356 SPDEKLEQERLAKGAVAVIKGA 381
|||||

DB 356 SPDEKLEQERLAKGAVAVIKGA 381
|||||

RESULT 14

heat shock protein 60 - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 12-Sep-1997
C:Accession: JN0601
R:Ohta, T.; Honda, K.; Kuroda, M.; Salto, K.; Hayashi, H.
Biochem. Biophys. Res. Commun. 193, 730-737, 1993
A:Title: Molecular characterization of the gene operon of heat shock proteins HSP60 and
A:Reference number: JN0600; MUID:93290669; PMID:7916607
A:Accession: JN0601
A:Molecule type: DNA

A:Residues: 1-539 <OH1>
A:Accession: PN0508
A:Molecule type: protein
A:Residues: 1-21 <OH2>
C:Genetics:
A:Gene: hsp60
C:Superfamily: chaperonin groEL
C:Keywords: heat shock; stress-induced protein

Query Match 4.8%; Score 26; DB 2; Length 539;
Best Local Similarity 100.0%; Pred. No. 3.6e-17;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 356 SPDEKLEQERLAKGAVAVIKGA 381
|||||

DB 357 SPDEKLEQERLAKGAVAVIKGA 382
|||||

RESULT 15

heat shock protein groEL (clone Rhz C) - Rhizobium meliloti
N:Alternate names: chaperonin groEL protein
C:Species: Rhizobium meliloti
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
C:Accession: JN0512
R:Rusanganwa, E.; Gupta, R.S.
Gene 126, 67-75, 1993
A:Title: Cloning and characterization of multiple groEL chaperonin-encoding genes in
A:Reference number: JN0509; MUID:93231539; PMID:8097179
A:Accession: JN0512
A:Molecule type: DNA
A:Residues: 1-541 <RUS>
A:Cross-References: GB:M94191; NID:9152236; PIDN:AAA26287.1; PID:9152238
C:Comment: This protein plays a role in protein folding and in the extracellular tr.
C:Genetics:
A:Gene: groEL
C:Superfamily: chaperonin groEL
C:Keywords: heat shock; molecular chaperone; stress-induced protein

Query Match 4.8%; Score 26; DB 2; Length 541;
Best Local Similarity 100.0%; Pred. No. 3.6e-17;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 273 AVKAPGFDGRRKAMLEDAITLTGTVI 298
|||||

DB 275 AVKAPGFDGRRKAMLEDAITLTGTVI 300
|||||

Search completed: April 8, 2003, 14:38:14
Job time : 50 secs